



RAW SEQUENCE LISTING

DATE: 04/12/2002

PATENT APPLICATION: US/09/714,792A

TIME: 11:40:35

Input Set : N:\Crf3\RULE60\09714792.raw

Output Set: N:\CRF3\04122002\I714792A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Collins, Mary
 6 Donaldson, Debra
 7 Fitz, Lori
 8 Neben, Tamlyn
 9 Whitters, Matthew
 10 Wood, Clive

12 (ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

14 (iii) NUMBER OF SEQUENCES: 9

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Genetics Institute, Inc.

18 (B) STREET: 87 CambridgePark Drive

19 (C) CITY: Cambridge

20 (D) STATE: MA

21 (E) COUNTRY: USA

22 (F) ZIP: 02140

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/714,792A

C--> 32 (B) FILING DATE: 16-Nov-2000

33 (C) CLASSIFICATION:

C--> 36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/609,572

38 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Brown, Scott A.

42 (B) REGISTRATION NUMBER: 32,724

43 (C) REFERENCE/DOCKET NUMBER: GI5268

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (617) 498-8224

47 (B) TELEFAX: (617) 876-5851

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 1525 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

ENTERED

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60 (iii) HYPOTHETICAL: NO
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 256..1404
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA AGATTGCTTG 60
72 CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA TAAGGAAGGA 120
74 AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG GTCTTGTGAT 180
76 AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA 240
78 CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT 291
79 Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
80 1 5 10
82 CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT 339
83 Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
84 15 20 25
86 CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT 387
87 Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
88 30 35 40
90 TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA 435
91 Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
92 45 50 55 60
94 CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG 483
95 Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
96 65 70 75
98 ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT 531
99 Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn
100 80 85 90
102 AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA 579
103 Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr
104 95 100 105
106 AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA 627
107 Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile
108 110 115 120
110 TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA 675
111 Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile
112 125 130 135 140
114 TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA 723
115 Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr
116 145 150 155
118 GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG 771
119 Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu
120 160 165 170
122 GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT 819
123 Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn
124 175 180 185
126 GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT 867
127 Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe
128 190 195 200
130 TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC 915

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131 Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser
132 205 210 215 220
134 TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA 963
135 Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu
136 225 230 235
138 TTC CTT CAT ATT AGT GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG 1011
139 Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp
140 240 245 250
142 AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT 1059
143 Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile
144 255 260 265
146 GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC 1107
147 Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn
148 270 275 280
150 GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT 1155
151 Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe
152 285 290 295 300
154 TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG 1203
155 Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp
156 305 310 315
158 AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC 1251
159 Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp
160 320 325 330
162 TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT 1299
163 Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu
164 335 340 345
166 TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA 1347
167 Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
168 350 355 360
170 TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT 1395
171 Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
172 365 370 375 380
174 ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG 1444
175 Thr Leu Cys
178 TCATATTAAA CTCAATTTCT CTAAAAATTT CGAATACATC TTCTTGAAAA TCCAAAAAAA 1504
180 AAAAAAAAAA AAAA ACTCGA G 1525
183 (2) INFORMATION FOR SEQ ID NO: 2:
185 (i) SEQUENCE CHARACTERISTICS:
186 (A) LENGTH: 383 amino acids
187 (B) TYPE: amino acid
188 (D) TOPOLOGY: linear
190 (ii) MOLECULE TYPE: protein
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
194 Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile Leu Leu Cys Thr
195 1 5 10 15
197 Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
198 20 25 30
200 Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys
201 35 40 45

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203  Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu
204      50                      55                      60
206  Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr
207      65                      70                      75                      80
209  Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
210                      85                      90                      95
212  Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu
213                      100                     105                     110
215  Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly
216                      115                     120                     125
218  Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp
219                      130                     135                     140
221  Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp
222                      145                     150                     155                     160
224  Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu
225                      165                     170                     175
227  Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys
228                      180                     185                     190
230  Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val
231                      195                     200                     205
233  Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe
234                      210                     215                     220
236  Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile
237                      225                     230                     235                     240
239  Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly
240                      245                     250                     255
242  Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu
243                      260                     265                     270
245  Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu
246                      275                     280                     285
248  Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys
249                      290                     295                     300
251  Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser
252                      305                     310                     315                     320
254  Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile
255                      325                     330                     335
257  Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu
258                      340                     345                     350
260  Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His
261                      355                     360                     365
263  Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys
264                      370                     375                     380

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266 (2) INFORMATION FOR SEQ ID NO: 3:

268 (i) SEQUENCE CHARACTERISTICS:

269 (A) LENGTH: 1369 base pairs

270 (B) TYPE: nucleic acid

271 (C) STRANDEDNESS: double

272 (D) TOPOLOGY: linear

274 (ii) MOLECULE TYPE: cDNA

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276 (iii) HYPOTHETICAL: NO
279 (ix) FEATURE:
280 (A) NAME/KEY: CDS
281 (B) LOCATION: 103..1245
284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
286 GGATCCGCGC GGATGAAGGC TATTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC 60
288 GCGGGGAGAG GAGGCAATAT CAAGGTTTAA AATCTCGGAG AA ATG GCT TTC GTT 114
289 Met Ala Phe Val
290 1
292 TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT 162
293 Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
294 5 10 15 20
296 GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG 210
297 Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
298 25 30 35
300 GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA 258
301 Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
302 40 45 50
304 TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA 306
305 Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
306 55 60 65
308 TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC 354
309 Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
310 70 75 80
312 ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC 402
313 Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
314 85 90 95 100
316 ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA 450
317 Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
318 105 110 115
320 TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA 498
321 Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro
322 120 125 130
324 CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC 546
325 Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr
326 135 140 145
328 AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT 594
329 Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu
330 150 155 160
332 CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT 642
333 Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
334 165 170 175 180
336 GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA 690
337 Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly
338 185 190 195
340 TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT 738
341 Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile
342 200 205 210
344 TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC 786

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VERIFICATION SUMMARY

DATE: 04/12/2002

PATENT APPLICATION: US/09/714,792A

TIME: 11:40:36

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L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:484 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:499 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:514 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:529 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:544 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9